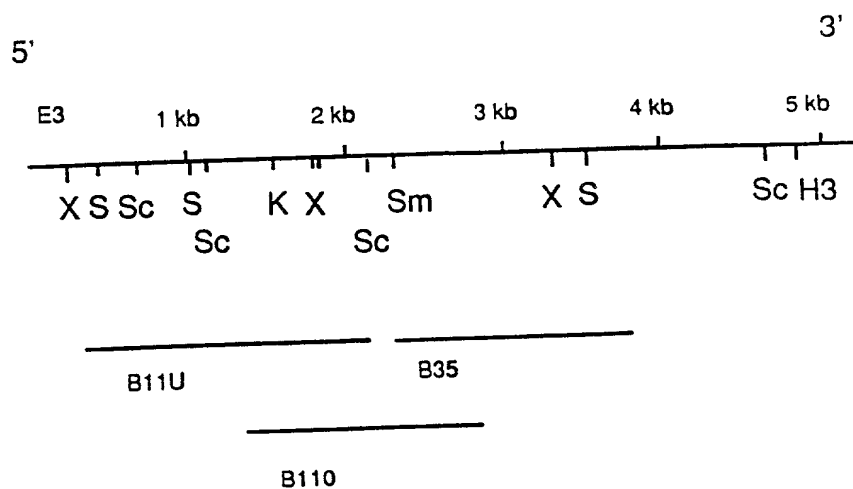


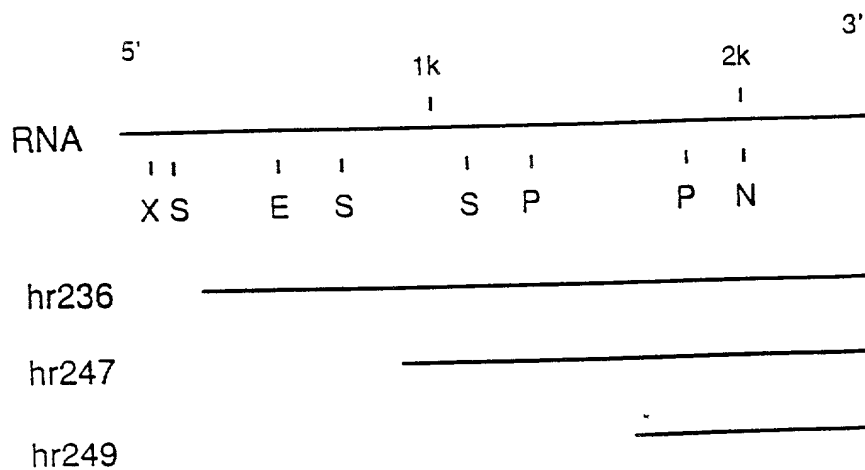
# Map of HaSV RNA 1 clones



H3=Hind3, K=Kpn1, Sc=Sac1, S=Sal1, Sm=Sma1, X=Xho1

FIG. 1a

# Map of HaSV RNA 2 clones



E=EcoR1, N=Not1, P=Pst1, S=Sal1. X=Xho1

FIG. 1b

10 30 50  
 GTTCTGCCCTCCCGACGGTAAATATAGGGGAACAAATGTACGCCGAAAGCGACAGACGTG  
 -----+-----+-----+-----+-----+-----+-----+  
 M Y A K A T D V  
 replicase start  
 70 90 110  
 GCGCGTGTCTACGCCGGCAGATGTGCCCTACGCCGAACGTACTGCAGCAGAGAGCAGTC  
 -----+-----+-----+-----+-----+-----+-----+  
 A R V Y A A A D V A Y A N V L Q Q R A V  
 130 150 170  
 AAGTTGGACTTCGCCCGCCCACTGAAGGCACTAGAAACCCCTCCACAGACTGTACTATCCG  
 -----+-----+-----+-----+-----+-----+-----+  
 K L D F A P P L K A L E T L H R L Y Y P  
 190 210 230  
 CTGCGCTTCAAGGGGCACTTTACCCCGACACACAACCCGATCCTGGCCGGGCACCAA  
 -----+-----+-----+-----+-----+-----+-----+  
 L R F K G G T L P P T Q H P I L A G H Q  
 250 270 290  
 CGTGTGCAGAGAGGTTCTGCACAAATTTCGCCAGGGGACGTAGCACAGTGTCTCGAGATA  
 -----+-----+-----+-----+-----+-----+-----+  
 R V A E E V L H N F A R G R S T V L E I

310 330 350  
GGGCCGTCCTGCACAGCGCACTTAAGCTACATGGGGCACCGAACGCCCCCGTCGCAGAC  
-----+-----+-----+-----+-----+-----+-----+  
G P S L H S A L K L H G A P N A P V A D  
  
370 390 410  
TATCACGGGTGCACCAAGTACGGCACCCGCGACGGCTCGGACACATTAAGGCTTAGAG  
-----+-----+-----+-----+-----+-----+-----+  
Y H G C T K Y G T R D G S R H I T A L E  
  
430 450 470  
TCTAGATCCGTGCGCACAGGCCCGCCGAGTTCAAGCCGACGCCCTCACTGCTCGCCAAC  
-----+-----+-----+-----+-----+-----+-----+  
S R S V A T G R P E F K A D A S L L A N  
  
490 510 530  
GGCATGGCTCCCGCACCTTCTGCGTCGACGGAGTCGGCTCTTGGCGGTTCAAAATCGCGC  
-----+-----+-----+-----+-----+-----+-----+  
G I A S R T F C V D G V G S C A F K S R  
  
550 570 590  
GTTGGAATTGCCAATCACTCCCTCTATGACGTGACCCCTAGAGGAGCTGGCCAATGCGTTT  
-----+-----+-----+-----+-----+-----+-----+  
V G I A N H S L Y D V T L E L A N A F

**FIG. 2 Cont'd**







1510 1530 1550  
CGAGTCCACTCGGAGACATAATCTGCAGCTCCGCCCTGTCCCTGAACAGGTCGGC  
-----+-----+-----+-----+-----+-----+-----+  
R V H S L G D I I C D V R L S P E Q V G  
  
1570 1590 1610  
TTCCCTGCCGTCGCCGTACCACTGCCCGCTCTTTCACGACAGGGAAGACTTGAGGTC  
-----+-----+-----+-----+-----+-----+-----+  
F L P S R V P P A R V F H D R E E L E V  
  
1630 1650 1670  
CTTCGCGAAGCTGGCTGCTACAACGAACGTCGGTACCTTCACCTCCTCTGTGGAGGAG  
-----+-----+-----+-----+-----+-----+-----+  
L R E A G C Y N E R P V P S T P P V E E  
  
1690 1710 1730  
CCCCAAGTTTCGACGCCGACTTGTGGCACGCGACCGGGCTCACTCCCCGAGTACCGC  
-----+-----+-----+-----+-----+-----+-----+  
P Q G F D A D L W H A T A A S L P E Y R  
  
1750 1770 1790  
GCCACCTTGACGGCAGGTCTCAACACCGACGTCAAGCAGCTCAAGATCACCCCTCGAGAAC  
-----+-----+-----+-----+-----+-----+-----+  
A T L Q A G L N T D V K Q L K I T L E N







2410 2430 2450  
CAGGAGGAAAGTCGCGCCACGGGCTGAGGGCGGATGACTGTGCACGAAGCGCAGGGA  
-----+-----+-----+-----+-----+-----+-----+  
Q E E K S R H G A E G A M T V H E A Q G  
2470 2490 2510  
CGCACTTTTGGCTGTCTCATTTCTGCAATTACACGGCTCCACAGCAGCAGCAAGCTCCTC  
-----+-----+-----+-----+-----+-----+-----+  
R T F A S V I L H Y N G S T A E Q K L L  
2530 2550 2570  
GCTGAGAAGTCGCACCTTCTAGTCGGCATCACGCGCCACACCAACCCTGTACATCCGC  
-----+-----+-----+-----+-----+-----+-----+  
A E K S H L L V G I T R H T N H L Y I R  
2590 2610 2630  
GACCCGACAGGTGACATTGAGAGACAATCAACCATAGCGGAAAGCCGAGGTGTTACA  
-----+-----+-----+-----+-----+-----+-----+  
D P T G D I E R Q L N H S A K A E V F T  
2650 2670 2690  
GACATCCCTGCACCCCTGGAGATCACGACTGTCAAACCGAGTGAAGAGTGCAGCGCAAC  
-----+-----+-----+-----+-----+-----+-----+  
D I P A P L E I T T V K P S E E V Q R N

FIG. 2 Cont'd





3310 3330 3350  
ATACTCGAGGAGATACTCCGTACCGGAGCCGCACGGTCCGGTACAGCAACGGTCTCCCC  
-----+-----+-----+-----+-----+-----+-----+  
I L E E I L R T G S R T V R Y S N G L P  
  
3370 3390 3410  
GACGAAGAAGAGGCCATGCTGCTCGAAGCGAAGATCAATCAAGTCCACACGCCACGTTCC  
-----+-----+-----+-----+-----+-----+-----+  
D E E E A M L L E A K I N Q V P H A T F  
  
3430 3450 3470  
GTCCTCGGCGGACTGGACCGAGTTTGACACCCGCCCAATAACACGAGTGAGCTGCTCTTC  
-----+-----+-----+-----+-----+-----+-----+  
V S A D W T E F D T A H N N T S E L L F  
  
3490 3510 3530  
GCCGCCCTTTAGAGCGCATCGGCACGCCTGCAGCTGCCGTTAATCTATTACAGAGAACGG  
-----+-----+-----+-----+-----+-----+-----+  
A A L L E R I G T P A A A V N L F R E R  
  
3550 3570 3590  
TGTGGGAAACGCACCTTGCAGCGAAGGCTCTAGGCTCCGTTGAAGTCGACGGTCTGCTC  
-----+-----+-----+-----+-----+-----+-----+  
C G K R T L R A K G L G S V E V D G L L

3610	3630	3650
GACTCCGGCAGCTTGGACGCTTGCCGCAACACCATCTTCTGCGCGTCATGCTC		
-----+	-----+	-----+
D S G A A W T P C R N T I F S A A V M L		
3670	3690	3710
ACGCTCTTCCGGCGGTCAAGTTCGACGCTTCAAGGCGACGACTCGCTCCTGTGGT		
-----+	-----+	-----+
T L F R G V K F A A F K G D D S L L C G		
3730	3750	3770
AGCCATTACCTCCGTTTCGACGCTAGCCGCCCTTCACATGGGGAACGTTACAAGACCAA		
-----+	-----+	-----+
S H Y L R F D A S R L H M G E R Y K T K		
3790	3810	3830
CATTGAAGTCGAGGTGCAGAAATCGTGCCGTACATCGGACTCCTCGTCTCCGCTGAG		
-----+	-----+	-----+
H L K V E V Q K I V P Y I G L L V S A E		
3850	3870	3890
CAGGTCGTCCTCGACCCCTGTCAGGAGCGCTCTCAAGATATTGGGCGCTGCTACAAGC		
-----+	-----+	-----+
Q V V L D P V R S A L K I F G R C Y T S		

FIG. 2 Cont'd







4450 4470 4490  
 GGAGACACCGCAAGACCAAGAGACTTGAACAGCAGAAAGCCCTTCGCAAGACAGG  
 -----+-----+-----+-----+-----+-----+  
 G D T A R T T E D L N S R K P P S Q D R  
 R H R K D H R R L E Q Q K A A F A R Q A

4510 4530 4550  
 CAATCACGCTGCTGAATGTCTGGACAGAAGCGGAGAAAGGACAGGAGTTCGTAACT  
 -----+-----+-----+-----+-----+-----+  
 Q S R S S E C L D R S G E R T G S S L T  
 I T L V \* M S G Q K R R K D R Q F V N C  
 P11b start

4570 4590 4610  
 GCCCCCACTGCTCCGAGCCCCCTCATTTCTCATTTTCGGAAAGAGCTCGACTGGCGACCGGG  
 -----+-----+-----+-----+-----+-----+  
 A P T A P S P S F S F S E R A R L A T G  
 P H C S E P L I L I F G K S S T G D R A

4630 4650 4670  
 CCGACTGTCGCGCTGCGACATCACCTTCGGCAACCCCATCCTGCGCCACGACGAGTT  
 -----+-----+-----+-----+-----+-----+  
 P T V A A A T S P S A T P S C A T D Q V  
 D C R R C D I T F G N P I L R H G P G C

FIG. 2 Cont'd

4690 4710 4730  
GCCGAGGACACGCCGACTTTGCGCCTTCTGGGTTCAGTCTGCCCGTCTGTC  
-----+-----+-----+-----+-----+-----+  
A A R T T P D F A P F L G S Q S A R A V  
R E D H A G L C A F P G F P V C P C C L

4750 4770 4790  
TCGAAGCCGTACCGGCCCCACGACTGCCCGTTGGAAGAAGTCACCCGCTCCACGC  
-----+-----+-----+-----+-----+-----+  
S K P Y R P P T T A R W K E V T P L H A  
E A V P A P H D C P L E R S H P A P R V

4810 4830 4850  
TGAAGGCGTGACCGGAGACCGACCGAAGTCAGGGAGGCCGAGACAGCGCGGTC  
-----+-----+-----+-----+-----+-----+  
W K G V T G D R P E V R E D P E T A A V  
E G R D R R P T G S Q G G P G D S G G R

4870 4890 4910  
GTCCAGGCTCTGATCAGCGCGCTTATCCTCAGAAGACGAAGCTTCTCCGACGATCC  
-----+-----+-----+-----+-----+-----+  
V Q A L I S G R Y P Q K T K L S S D A S  
P G S D Q R P L S S E D E A F L R R I Q

4930 4950 4970  
AAAGGCTACTCAAGAACTAAGGATGCTCACAATCCACCTCTTTCTCCCGAGTGCG  
-----+-----+-----+-----+-----+-----+-----+  
K G Y S R T K G C S Q S T S F P A P S A  
R L L K N \* M L T I H L F S C P E C G  
P14 start  
4990 5010 5030  
GATTACGAGCCGCGACTGCCAGACAGTCCGAGTCTGCCGCCGCTGCAGAGATGGCG  
-----+-----+-----+-----+-----+-----+-----+  
D Y Q A R D C Q T V R V C R A A A E M A  
L P G P R L P D S P S L P R R C R D G A  
5050 5070 5090  
CGCTCATGTATTCAGAGCCGTTGGCTTCATCTGCCGCCAGTGCCGACTTGAAGCGCATA  
-----+-----+-----+-----+-----+-----+-----+  
R S C I H E P L A S S A A S A D L K R I  
L M Y S R A V G F I C R Q C R L E A H T  
5110 5130 5150  
CGCTCTACCTCGGACTCTGTTCCTCCGATGTAAAGATCAGCAAGAGCGCATGAAGGAACAAA  
-----+-----+-----+-----+-----+-----+-----+  
R S T S D S V P D V K I S K S A \*  
L Y L G L C S R C K D Q Q E R M K E Q N

**FIG. 2 Cont'd**

5170 5190 5210  
 ATTAGTTTCCTTGTTTCGTAACAAGGTGGTCCCTCCCATGAGGTAAGACTCTGGTGAG  
 -----+-----+-----+-----+-----+-----+-----+  
 \*

5230 5250 5270  
 TCCTCAACGTTACTCGTTGAGTCTGCTGCGGTTGATTCCATTCCCAAGCAGCAAAGGT  
 -----+-----+-----+-----+-----+-----+-----+  
 -----+-----+-----+-----+-----+-----+-----+

5290 5310  
 GCGCAACTAGTACGGCGCCCCCTGGGATACCA  
 -----+-----+-----+-----+-----+-----+-----+

FIG. 2 Cont'd



```

370                               390                               410
GCAGGATGGGAGATGCTGGAGTGGCGTCACAGCGACCTCACAAACCGTCGCGGAACCCGTA
-----+-----+-----+-----+-----+-----+-----+
A G W E M L E W R H S D L T T V A E P V
      M G D A G V A S Q R P H N R R G T R N
      P71 start

430                               450                               470
ACGTTCCGGTCAGCGCCAACACCGTCACCGTCAATGGTAGAAGAAACCAACGCGTCGGA
-----+-----+-----+-----+-----+-----+-----+
T F G S A P T P S P S M V E E T N G V G
      V R V S A N T V T V N G R R N Q R R R T

490                               510                               530
CCGGAAGGCAAGTTTCTCCCCCTGACAAATTTACCGCTGCTGCACAAGACCTCGCGCAA
-----+-----+-----+-----+-----+-----+-----+
P E G K F L P L T I S P L L H K T S R K
      G R Q V S P P D N F T A A A Q D L A Q S

550                               570                               590
GCCTTGACGCCAACCGTCACCTTCCCCCGCTAACATCTCTAGCATGCCCGAATTCGGA
-----+-----+-----+-----+-----+-----+-----+
A L T P T P S L S P L T S L A C P N S G
      L D A N T V T F P A N I S S M P E F R N

```

FIG. 3a Cont'd













**FIG. 3 a Cont'd**





370	390	410
GCAGGATGGGAGATGCTGGAGTGGCGTCACAGCGACCTCACAACCGTCGCGGAACCCGTA		
-----+	-----+	-----+
A G W E M L E W R H S D L T T V A E P V		
430	450	470
ACGTTCCGGTCAGCGCCAACACCGTCACCGTCAATGGTAGAAGAAACCAACGGCGTCGGA		
-----+	-----+	-----+
T F G S A P T P S P S M V E E T N G V G		
490	510	530
CCGGAAGGCAAGTTTCTCCCCCTGACAAATTTCACCGCTGCTGCACAAGACCTCGCGCAA		
-----+	-----+	-----+
P E G K F L P L T I S P L L H K T S R K		
550	570	590
GCCTTGACGCCAACACCGTCACTTTCGCCCGCTAACATCTCTAGCATGCCCGAATTCCGG		
-----+	-----+	-----+
A L T P T P S L S P A N I S S M P E F R		
610	630	650
AATTGGCCAAAGGAAAGATCGACCTCGACTCCGATTCATCCGCTGGTGTACTTCAAGTAC		
-----+	-----+	-----+
N W A K G K I D L D S D S I G W Y F K Y		

Fig. 3b (cont'd)

	670	690	710
	CTTGACCCAGCGGTGCTACAGAGTCTGC	GCGCGCGTAGTACTCGAAGATCCCT	
	L D P A G A T E S A R A V G E Y S K I P		
	730	750	770
	GACGGCCTCGTCAAGTTCTCCGTGACG	CAGAGATAAGAGAGATCTATAACGAGGAGTGC	
	D G L V K F S V D A E I R E I Y N E E C		
	790	810	830
	CCCGTCGTCAC TGACGTGCCGTCCCCCTCGAC	GCGCCGCGCAGTGGAGCCTCTCGATTTC	
	P V V T D V S V P L D G R Q W S L S I F		
	850	870	890
	TCCTTCCGATGTTCAGAACC	GCTACGTGCGCGTAGCGAACGTCGAGAAACAAGGAGATG	
	S F P M F R T A Y V A V A N V E N K E M		
	910	930	950
	TCGCTCGACGTTGTCAACGACCTCATCGAGT	GCTCAACAATCTCGCCGACTGGCGTTAT	
	S L D V V N D L I E W L N N L A D W R Y		



970	990	1010
GTCGTTGACTCTGAACAGTGGATTAACTTCACCAATGACACCACTAGTACTAGTCCGCATC		
-----+	-----+	-----+
V V D S E Q W I N F T N D T T Y Y V R I		
1030	1050	1070
CGCGTTCTACGTCCAACCTACGACGTTCCAGACCCACAGAGGGCCTTGTTTCGCACAGTC		
-----+	-----+	-----+
R V L R P T Y D V P D P T E G L V R T V		
1090	1110	1130
TCAGACTACCGCCTCACTTATAAGGCGGATAACATGTGAAGCCAACATGCCAACAATCGTC		
-----+	-----+	-----+
S D Y R L T Y K A I T C E A N M P T L V		
1150	1170	1190
GACCAAGGCTTTTGATCGGGCCAGTACGCTCTCACCCCGACTAGCCTACCGCAGTAC		
-----+	-----+	-----+
D Q G F W I G G Q Y A L T P T S L P Q Y		
1210	1230	1250
GACGTCAGCGGCGCTACGCTCTGCACACTTTGACCTTCGCCAGACCATCCAGCGCGCT		
-----+	-----+	-----+
D V S E A Y A L H T L T F A R P S S A A		

Fig. 3b (cont'd)

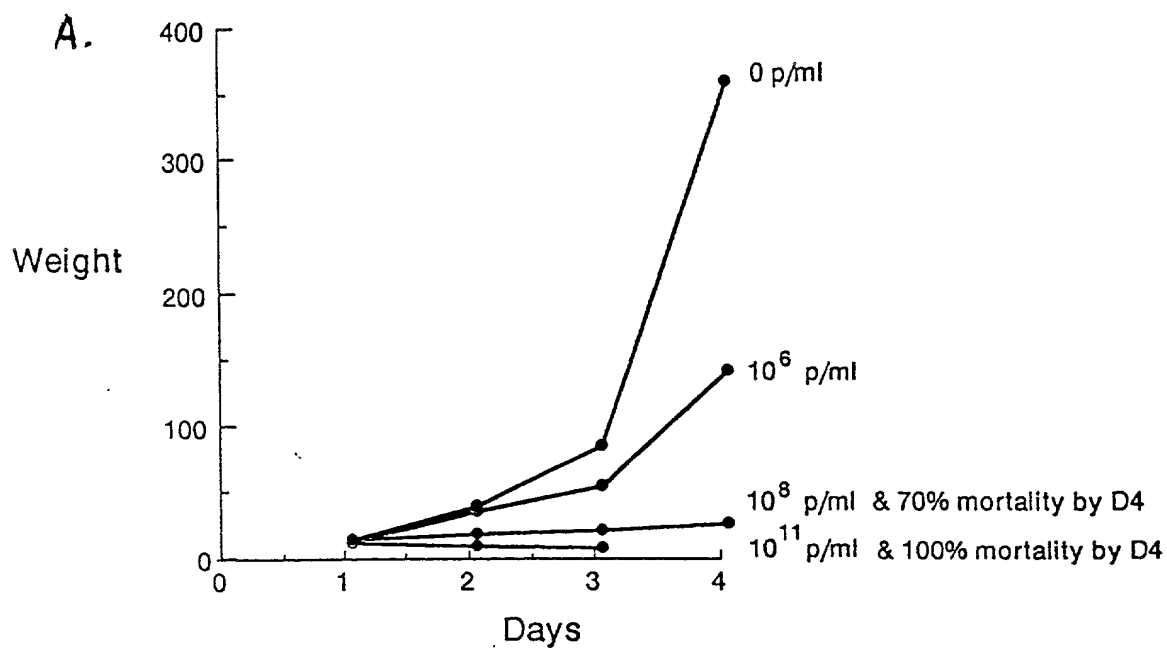
[illegible]

Fig. 3b (cont'd)

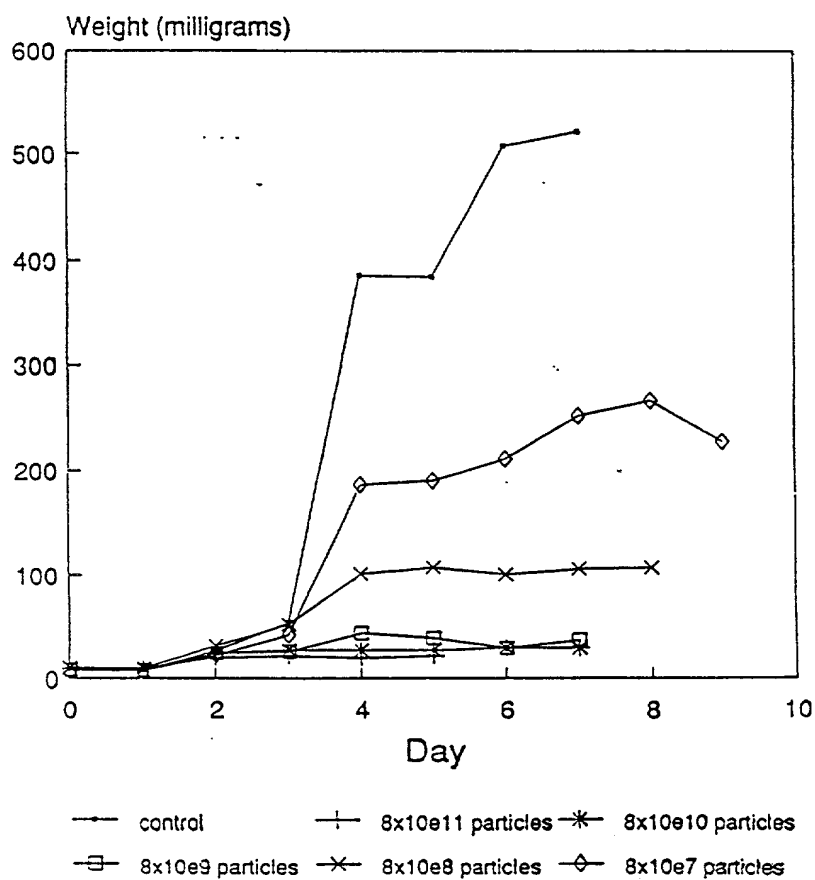
2170	2190	2210
TCCATCATCAAGTCCGTGGCGAGACTGCCGTGGCGGCTCAGTCCGGCTCGCGAAG		
-----+	-----+	-----+
S I I K S V G E T A V G A A Q S G L A K		
2230	2250	2270
CTACCCGGACTGCTAATGAGTGTAACAGGAAGATTGCCGCGGTGTCCGCGCGCCGA		
-----+	-----+	-----+
L P G L L M S V P G K I A A R V R A R R		
2290	2310	2330
GCGCGCCGCGCGCTCGTGCCAAATTAGTTTGCTCGCTCCTGTTTCGCCGTTTCGTAA		
-----+	-----+	-----+
A R R R A A R A N *		
2350	2370	2390
AACGGCGTGGTCCCGCACATTACGCGTACCCTAAAGACTCTGGTGAGTCCCGTCGTTAC		
-----+	-----+	-----+
2410	2430	2450
ACGACGGGTCTGCCGCGGTTCGATTCCATTCCCAAGCGGCAAGAGACGTAGTAGCTC		
-----+	-----+	-----+
2470		
TGCGTCCCTCGGGATACCA		
-----+		

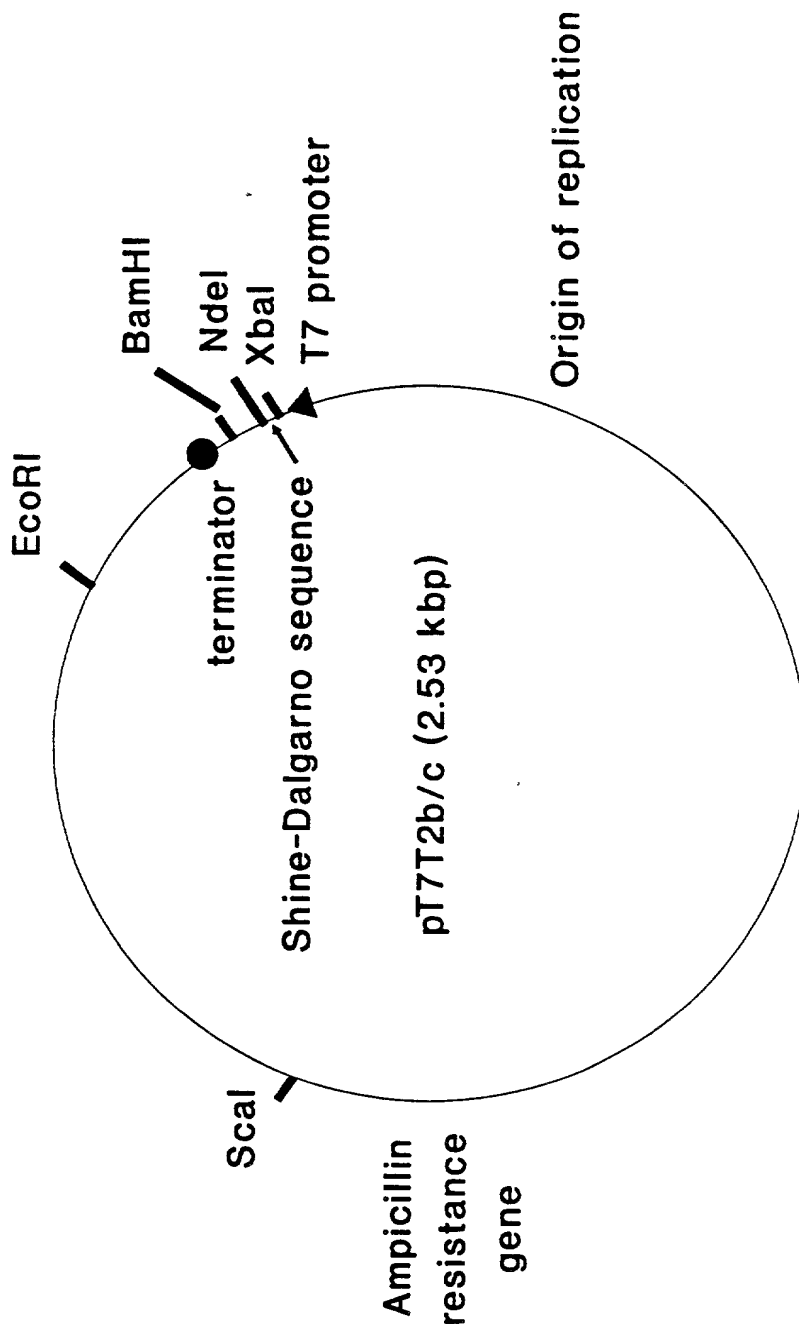
Fig. 3b (cont'd)

FIG. 4



B Weight gain of infected larvae





# Proteins encoded by the HaSV genome

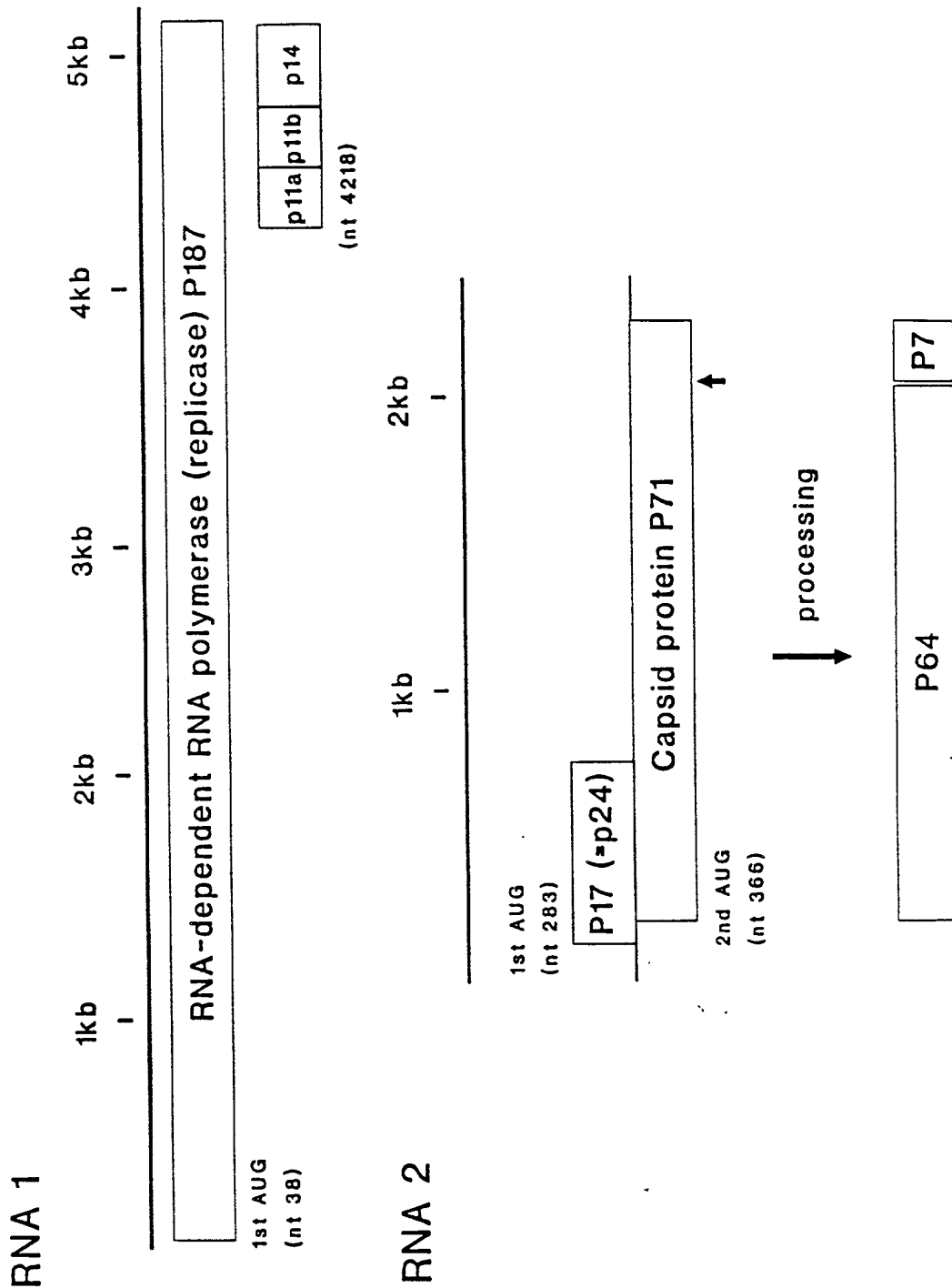


FIG. 6



# PROTEINS EXPRESSED FROM HaSV RNA 2

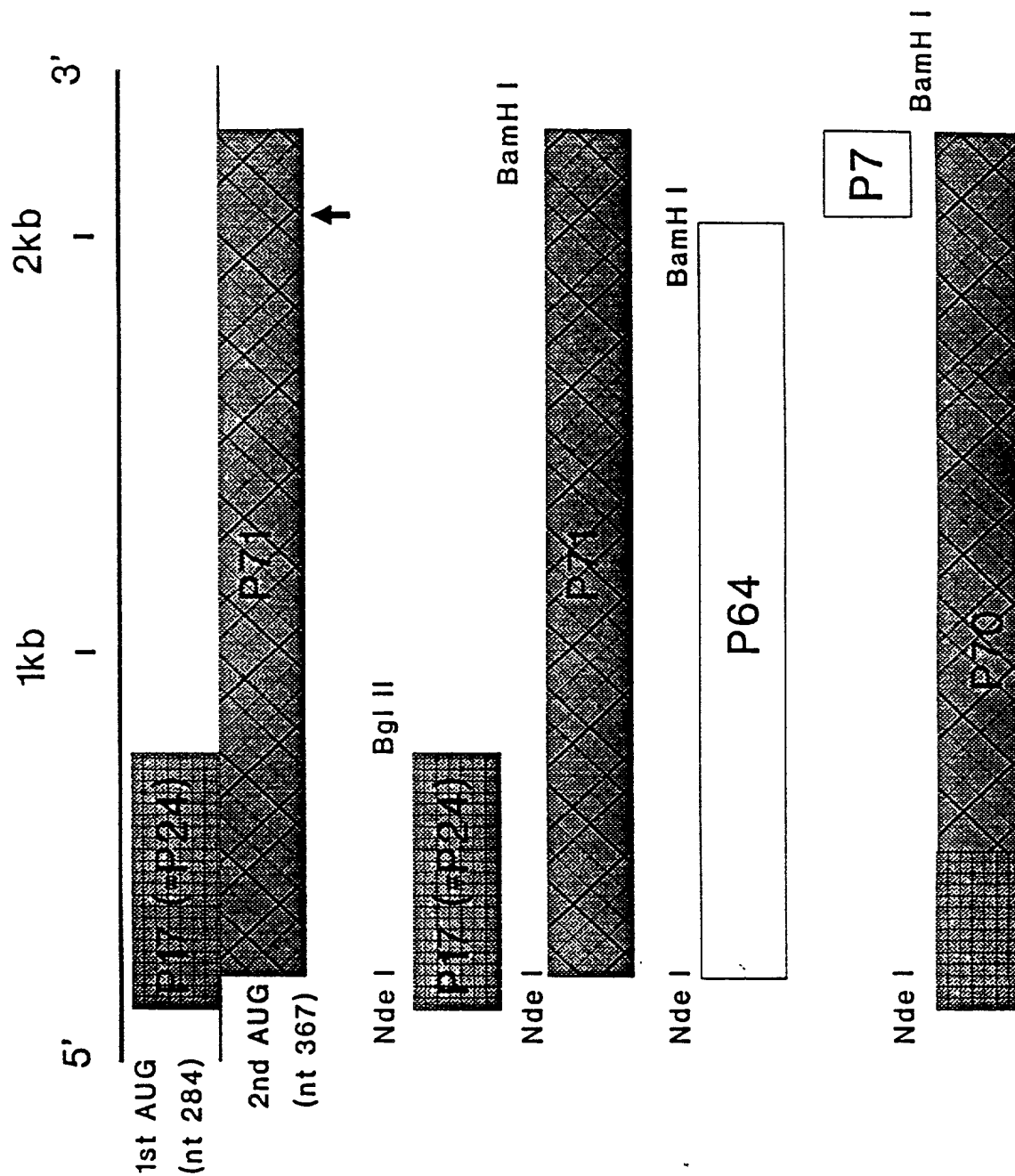
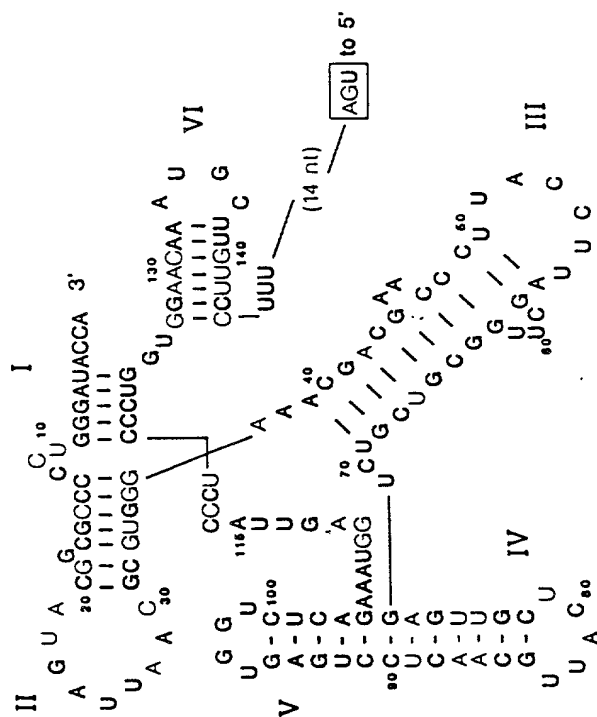


FIG. 7

# HaSV RNA 3' - terminal tRNA-like structures

## RNA 1



## RNA 2

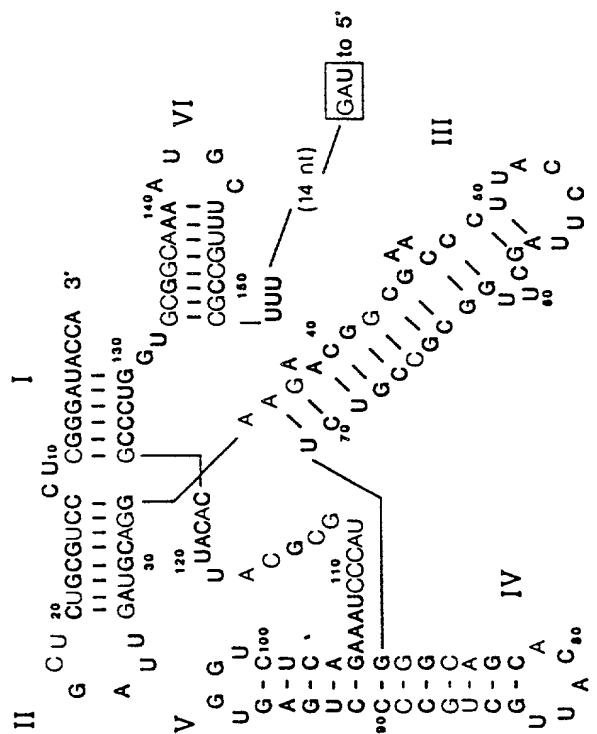
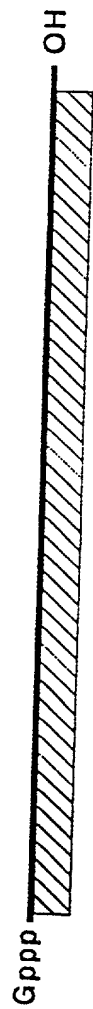
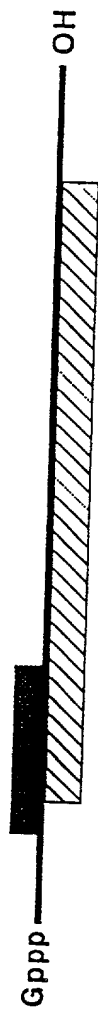


FIG. 8

# HaSV RNA1



# HaSV RNA2



## Insect cell expression constructs

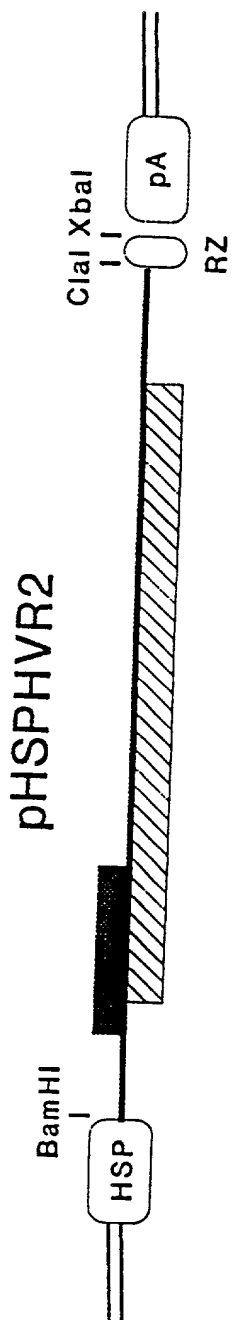
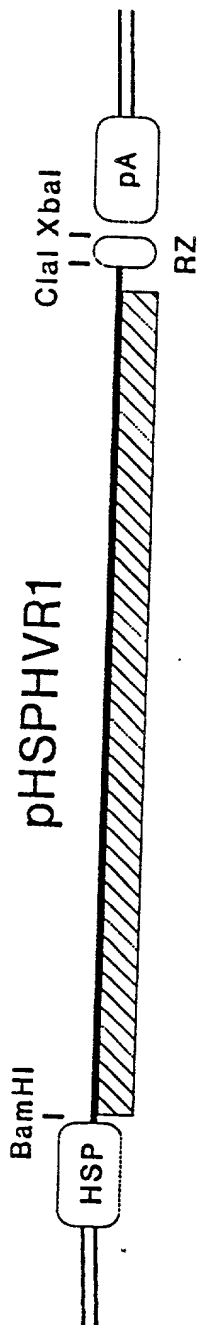
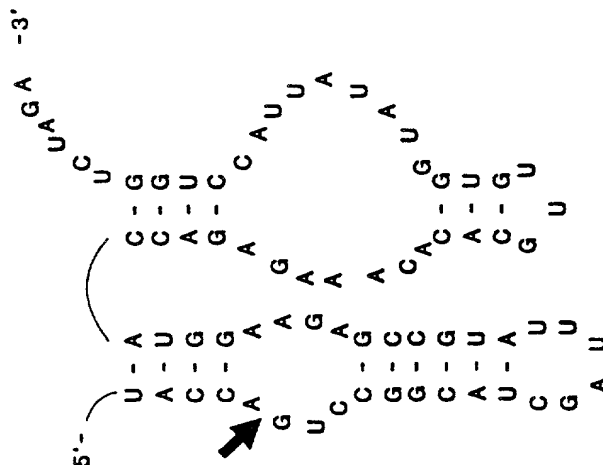


Fig. 9

# CIS-ACTING RIBOZYMES FOR HASV 3' ENDS

## HAIRPIN



## HEPATITIS DELTA VIRUS

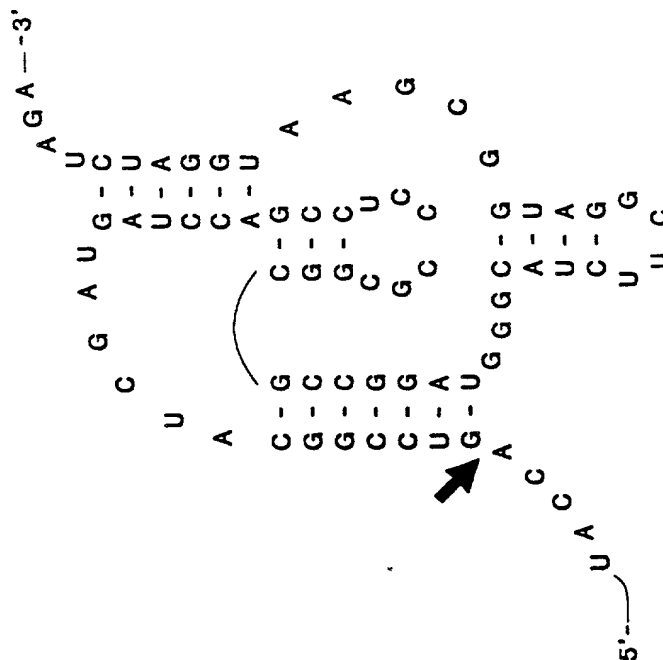
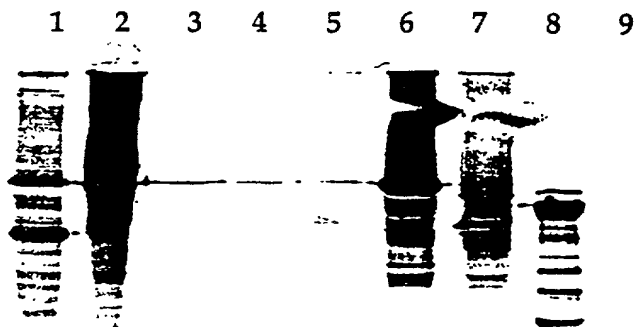


FIG. 10

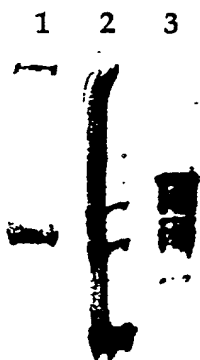
FIG. 11

WESTERN BLOTS OF HaSV CAPSID PROTEIN

A. HaSV ANTISERUM



B. HaSV ANTISERUM



C. Bt ANTISERUM

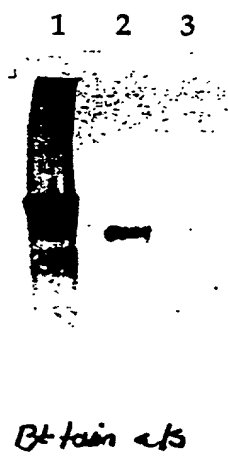
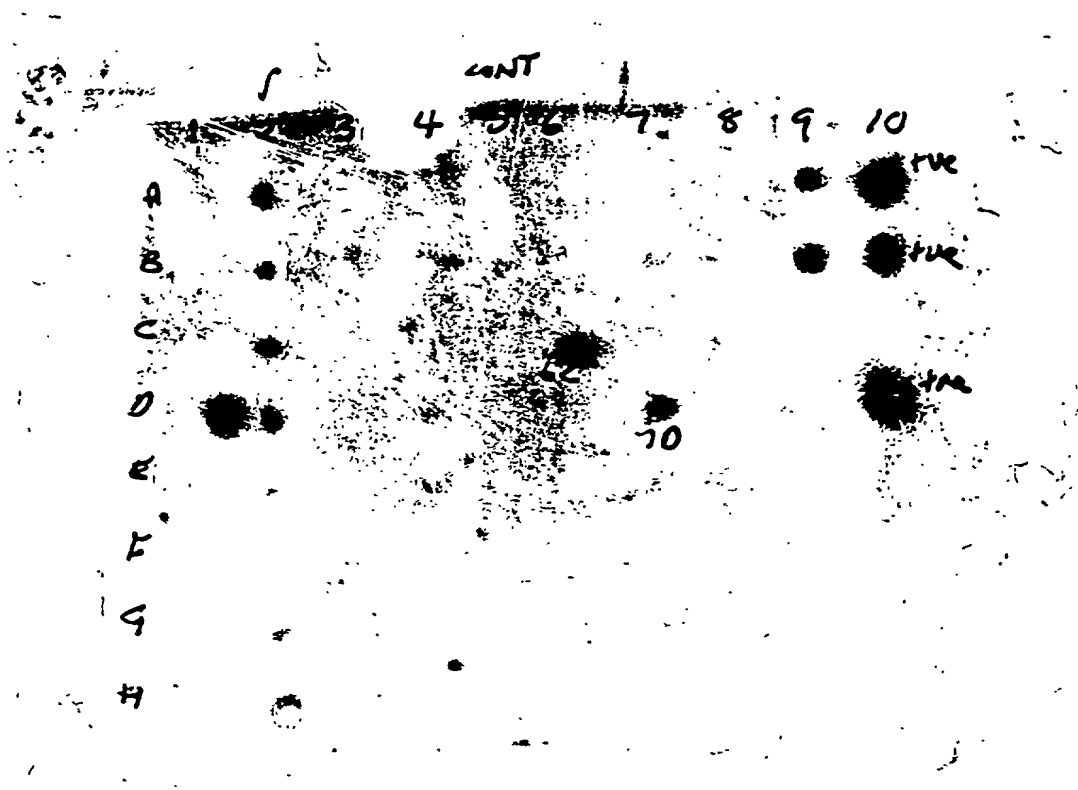


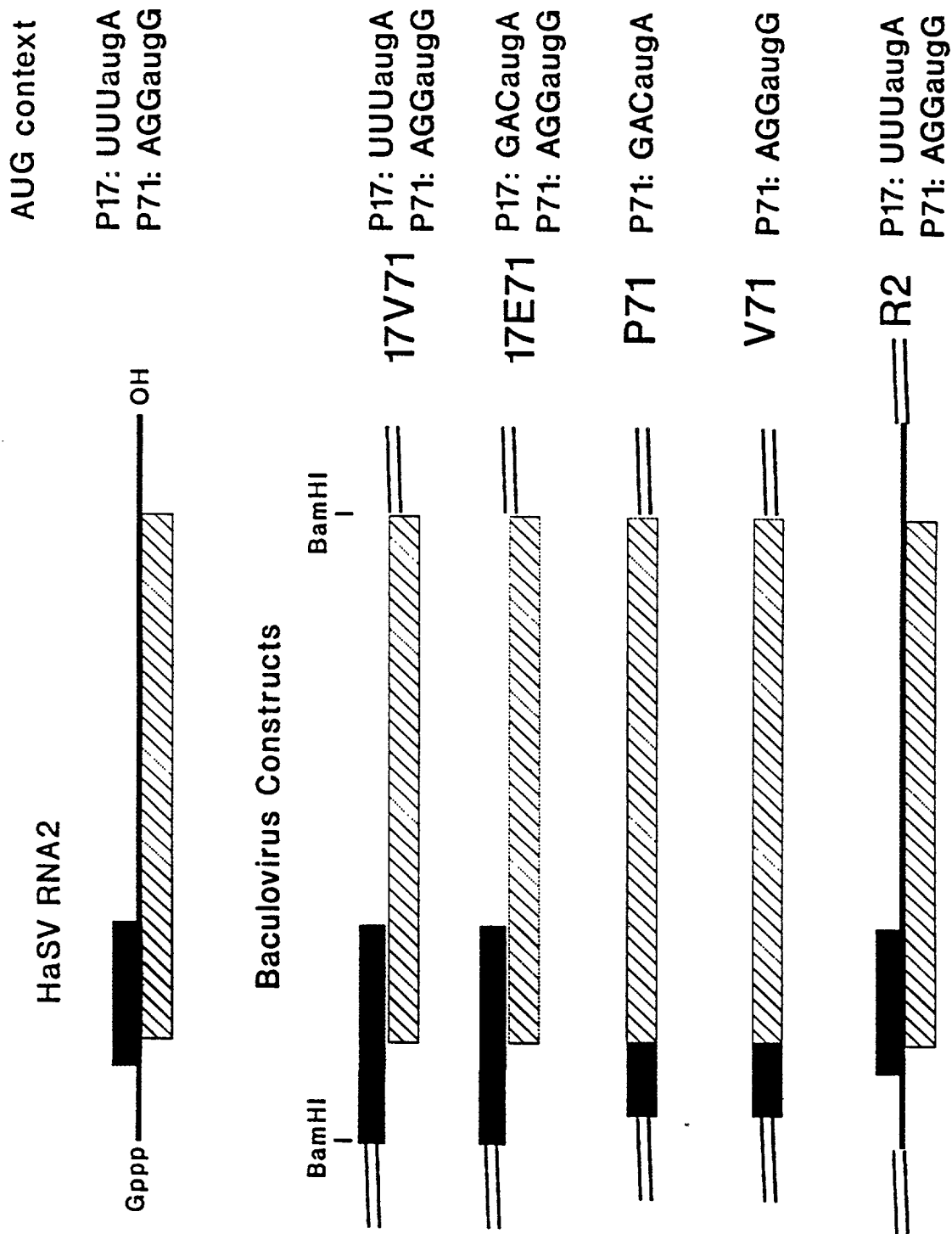
FIG. 12

DOT-BLOT DETECTION OF HaSV IN FIELD-COLLECTED  
HELICOVERPA LARVAE



0991262 112001

Fig. 13



transgenic plant genome:

P71 capsid protein

(P7)

capsotoxin fusion

proteins:

P71

FIG. 14a

capsoids assembled:

virus capsoid strategy:  
capsotoxin encapsulation

capsoids enter feeding larvae  
and disassembled:

releasing active, insect-specific toxin

HaSV RNA 1

HaSV RNA 2

replicase

P17

capsid protein

transgenic plant genome:

replicase

(a/s?) toxin

capsid protein

transcripts:

replicase

(a/s?) toxin

proteins:

FIG. 14b

capsoids assembled:

virus capsoid strategy:  
toxin message encapsulation  
and amplification

capsoids enter and infect feeding larvae

capsoids disassembled:

replicase

(a/s?) toxin

mRNA amplification and expression and secretion of toxin



# Virus expression in plants: the one-way vector

FIG. 14c

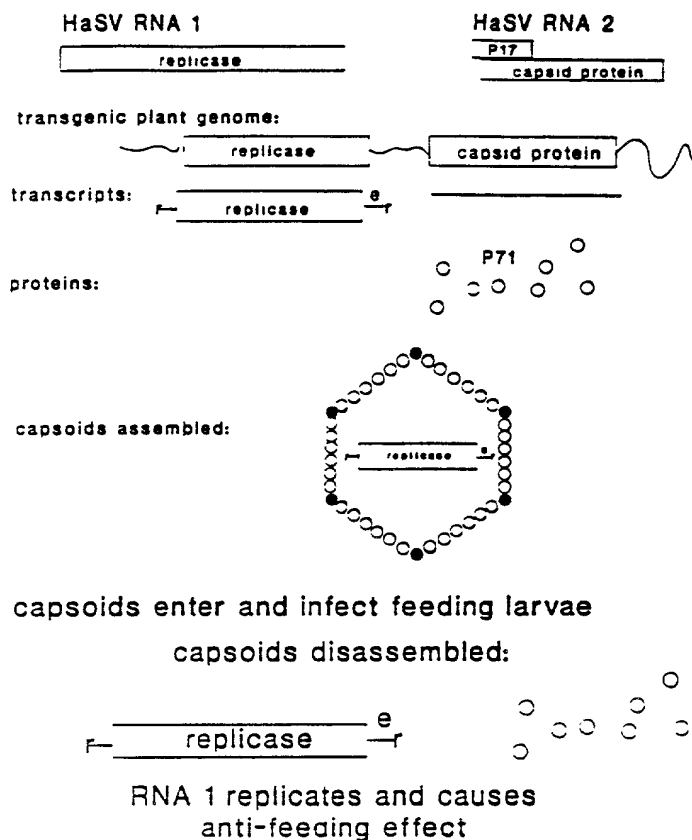
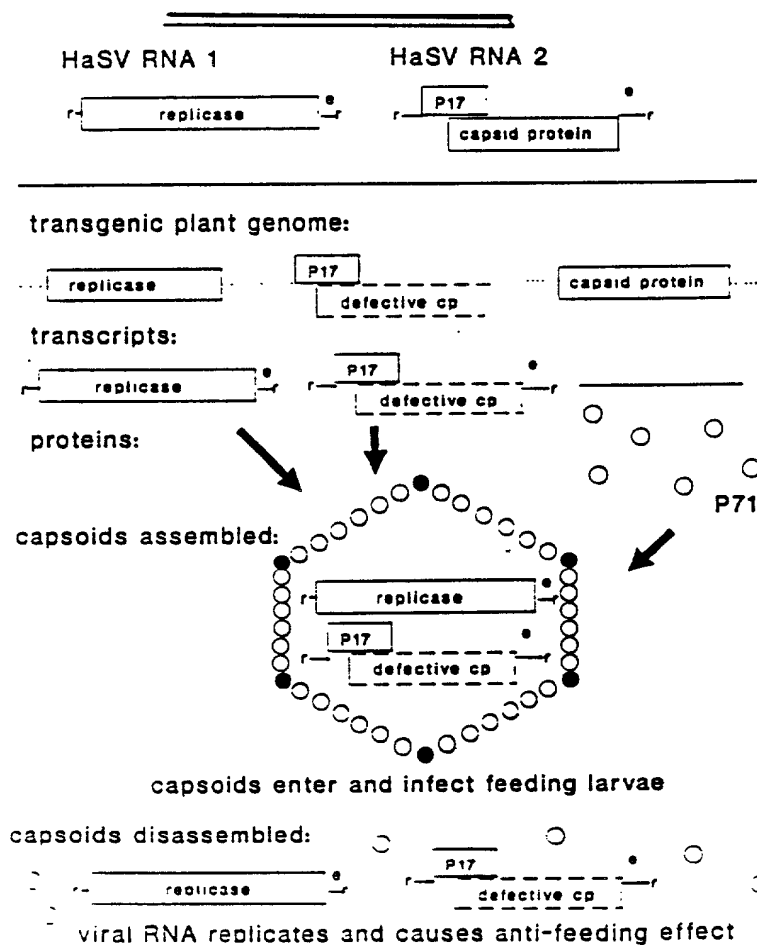
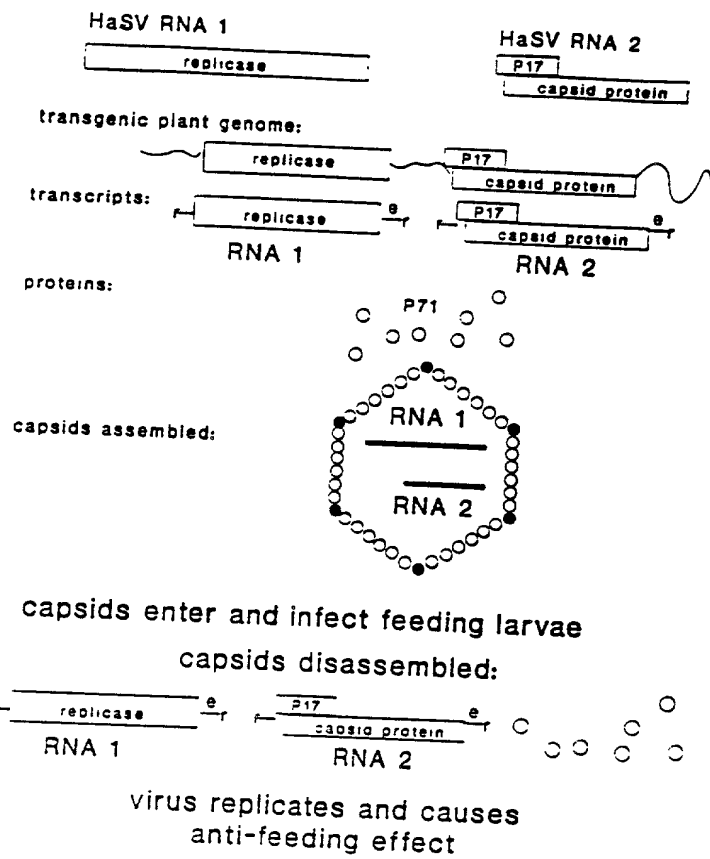


FIG. 14d



# virus expression in plants:

FIG. 14e



## virus expression in plants: the one-way vector for a toxin

FIG. 14f

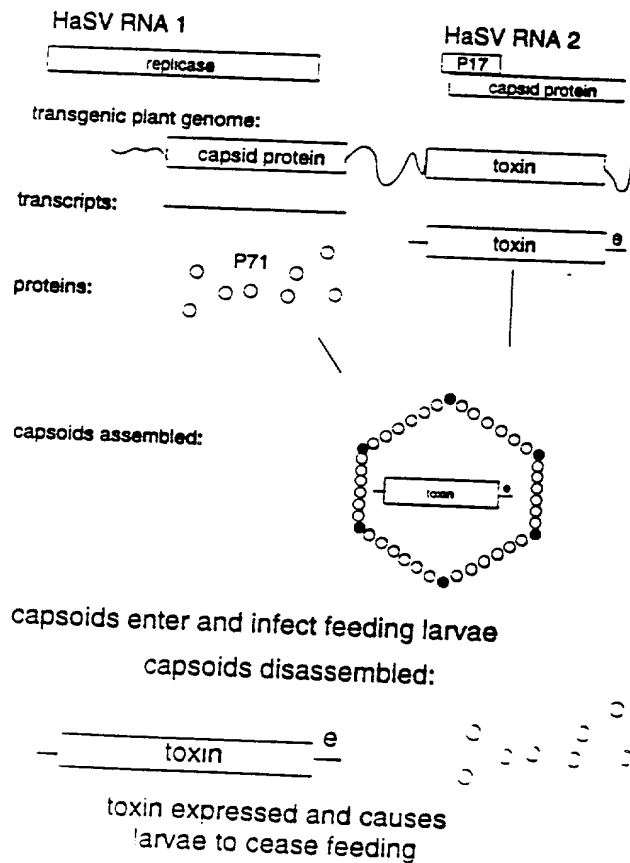


Fig. 15

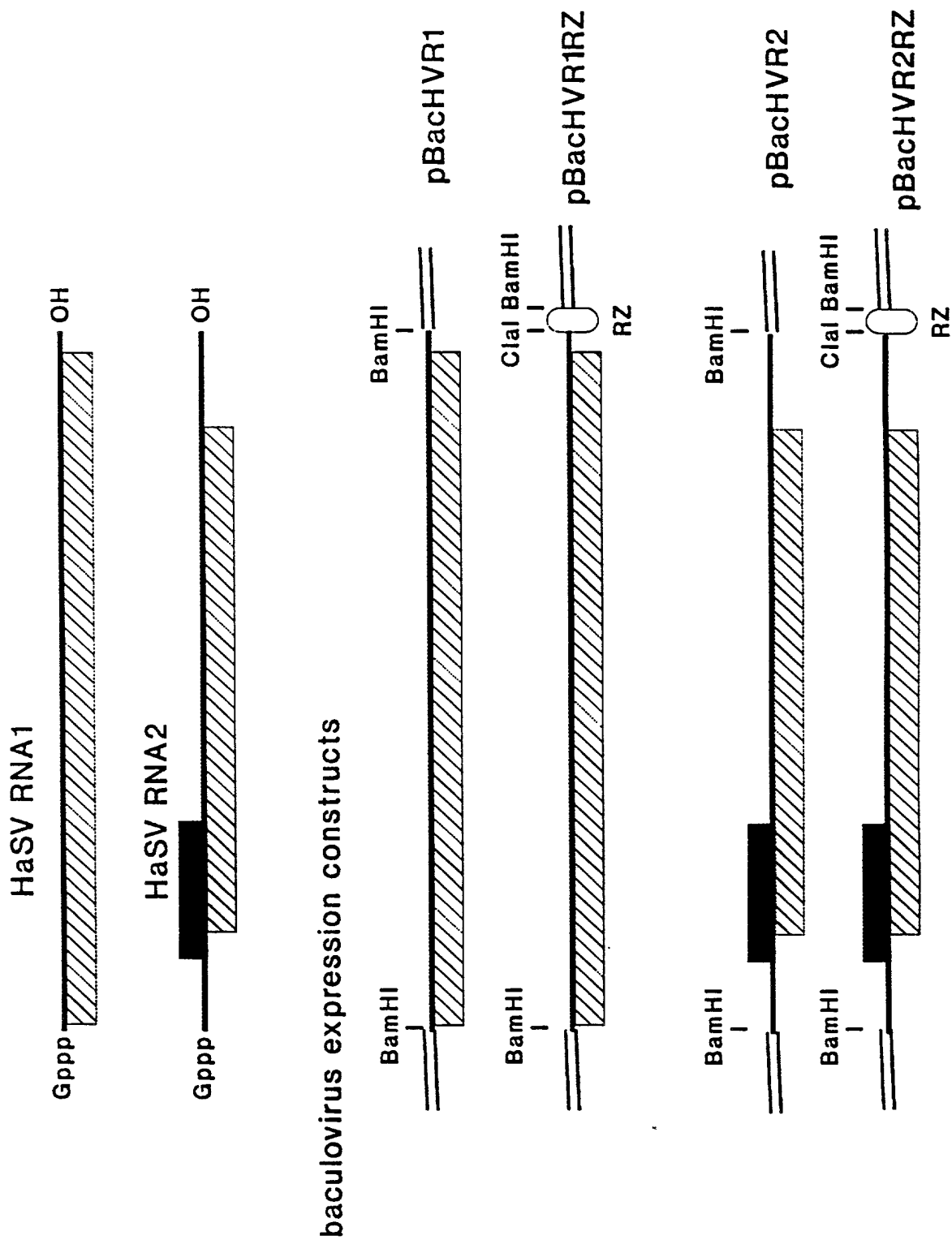
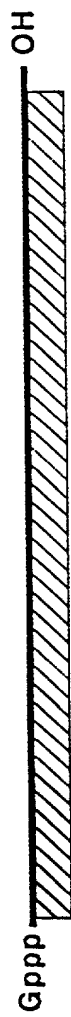


Fig. 16

### HaSV RNA1



### HaSV RNA2



### Protoplast expression constructs

